

Report: us-10-058-422-1.rng

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[illegible]

[illegible][illegible]

RESULTS AND DISCUSSION

AAStt, 2211:

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117
117

Figure 1. The effect of the concentration of the Fe^{2+} solution on the adsorption of Fe^{2+} by the Fe^{2+} -loaded adsorbent. The concentration of the Fe^{2+} solution was 0.01, 0.02, 0.05, 0.1, 0.2, 0.5, 1, 2, 5, 10, 20, 50, 100, 200, 500, 1000, 2000, 5000, 10000, 20000, 50000, 100000, 200000, 500000, 1000000, 2000000, 5000000, 10000000, 20000000, 50000000, 100000000, 200000000, 500000000, 1000000000, 2000000000, 5000000000, 10000000000, 20000000000, 50000000000, 100000000000, 200000000000, 500000000000, 1000000000000, 2000000000000, 5000000000000, 10000000000000, 20000000000000, 50000000000000, 100000000000000, 200000000000000, 500000000000000, 1000000000000000, 2000000000000000, 5000000000000000, 10000000000000000, 20000000000000000, 50000000000000000, 100000000000000000, 200000000000000000, 500000000000000000, 1000000000000000000, 2000000000000000000, 5000000000000000000, 10000000000000000000, 20000000000000000000, 50000000000000000000, 100000000000000000000, 200000000000000000000, 500000000000000000000, 1000000000000000000000, 2000000000000000000000, 5000000000000000000000, 10000000000000000000000, 20000000000000000000000, 50000000000000000000000, 100000000000000000000000, 200000000000000000000000, 500000000000000000000000, 1000000000000000000000000, 2000000000000000000000000, 5000000000000000000000000, 10000000000000000000000000, 20000000000000000000000000, 50000000000000000000000000, 100000000000000000000000000, 200000000000000000000000000, 500000000000000000000000000, 1000000000000000000000000000, 2000000000000000000000000000, 5000000000000000000000000000, 10000000000000000000000000000, 20000000000000000000000000000, 50000000000000000000000000000, 100000000000000000000000000000, 200000000000000000000000000000, 500000000000000000000000000000, 1000000000000000000000000000000, 2000000000000000000000000000000, 5000000000000000000000000000000, 10000000000000000000000000000000, 20000000000000000000000000000000, 50000000000000000000000000000000, 100000000000000000000000000000000, 200000000000000000000000000000000, 500000000000000000000000000000000, 1000000000000000000000000000000000, 2000000000000000000000000000000000, 5000000000000000000000000000000000, 10000000000000000000000000000000000, 20000000000000000000000000000000000, 50000000000000000000000000000000000, 100000000000000000000000000000000000, 200000000000000000000000000000000000, 500000000000000000000000000000000000, 1000000000000000000000000000000000000, 2000000000000000000000000000000000000, 5000000000000000000000000000000000000, 10000000000000000000000000000000000000, 20000000000000000000000000000000000000, 50000000000000000000000000000000000000, 100000000000000000000000000000000000000, 200000000000000000000000000000000000000, 500000000000000000000000000000000000000, 1000000000000000000000000000000000000000, 2000000000000000000000000000000000000000, 5000000000000000000000000000000000000000, 100, 200, 500, 1000, 2000, 5000, 100, 200, 500, 1000, 2000, 5000, 100, 200, 500, 1000, 2000, 5000, 100, 200, 500, 1000, 2000, 5000, 100, 200, 500, 100000000

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 \mathcal{G}
 \mathcal{F}
 \mathcal{E}
 \mathcal{D}
 \mathcal{C}
 \mathcal{B}
 \mathcal{A}

[illegible]
$$\frac{d}{dt} \left(\frac{1}{2} \dot{x}^2 + \frac{1}{2} \dot{y}^2 + \frac{1}{2} \dot{z}^2 \right) = \dot{x} \ddot{x} + \dot{y} \ddot{y} + \dot{z} \ddot{z}$$

$\frac{1}{2} \times \frac{1}{2} = \frac{1}{4}$

[illegible][illegible]

100

100

100% Sequence 200 bp: 46 A; 69 C; 63 G; 40 T; 0 other:									
Score: 100.00; Score 20; 19 22; Length 200:									
Mismatch: 0; Conservation: 100.00; Pred. No. 12; Mismatches: 0; Gaps: 0;									
1	1	GAATGATGAGAAATGAA	20						
2	1	GAATGATGAGAAATGAA	20						
3	1	GAATGATGAGAAATGAA	20						
4	1	GAATGATGAGAAATGAA	20						
5	1	GAATGATGAGAAATGAA	20						
6	1	GAATGATGAGAAATGAA	20						
7	1	GAATGATGAGAAATGAA	20						
8	1	GAATGATGAGAAATGAA	20						
9	1	GAATGATGAGAAATGAA	20						
10	1	GAATGATGAGAAATGAA	20						
11	1	GAATGATGAGAAATGAA	20						
12	1	GAATGATGAGAAATGAA	20						
13	1	GAATGATGAGAAATGAA	20						
14	1	GAATGATGAGAAATGAA	20						
15	1	GAATGATGAGAAATGAA	20						
16	1	GAATGATGAGAAATGAA	20						
17	1	GAATGATGAGAAATGAA	20						
18	1	GAATGATGAGAAATGAA	20						
19	1	GAATGATGAGAAATGAA	20						
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21	1	GAATGATGAGAAATGAA	20						
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65	1	GAATGATGAGAAATGAA	20						
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67	1	GAATGATGAGAAATGAA	20						
68	1	GAATGATGAGAAATGAA	20						
69	1	GAATGATGAGAAATGAA	20						
70	1	GAATGATGAGAAATGAA	20						
71	1	GAATGATGAGAAATGAA	20						
72	1	GAATGATGAGAAATGAA	20						
73	1	GAATGATGAGAAATGAA	20						
74	1	GAATGATGAGAAATGAA	20						
75	1	GAATGATGAGAAATGAA	20						
76	1	GAATGATGAGAAATGAA	20						
77	1	GAATGATGAGAAATGAA	20						
78	1	GAATGATGAGAAATGAA	20						
79	1	GAATGATGAGAAATGAA	20						
80	1	GAATGATGAGAAATGAA	20						
81	1	GAATGATGAGAAATGAA	20						
82	1	GAATGATGAGAAATGAA	20						
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XX	1	SEI	2	SEI	3	SEI	4	SEI	5	SEI	6	SEI	7	SEI	8	SEI	9	SEI	10	SEI	11	SEI	12	SEI	13	SEI	14	SEI	15	SEI	16	SEI	17	SEI	18	SEI	19	SEI	20	SEI	21	SEI	22	SEI	23	SEI	24	SEI	25	SEI	26	SEI	27	SEI	28	SEI	29	SEI	30	SEI	31	SEI	32	SEI	33	SEI	34	SEI	35	SEI	36	SEI	37	SEI	38	SEI	39	SEI	40	SEI	41	SEI	42	SEI	43	SEI	44	SEI	45	SEI	46	SEI	47	SEI	48	SEI	49	SEI	50	SEI	51	SEI	52	SEI	53	SEI	54	SEI	55	SEI	56	SEI	57	SEI	58	SEI	59	SEI	60	SEI	61	SEI	62	SEI	63	SEI	64	SEI	65	SEI	66	SEI	67	SEI	68	SEI	69	SEI	70	SEI	71	SEI	72	SEI	73	SEI	74	SEI	75	SEI	76	SEI	77	SEI	78	SEI	79	SEI	80	SEI	81	SEI	82	SEI	83	SEI	84	SEI	85	SEI	86	SEI	87	SEI	88	SEI	89	SEI	90	SEI	91	SEI	92	SEI	93	SEI	94	SEI	95	SEI	96	SEI	97	SEI	98	SEI	99	SEI	100	SEI	101	SEI	102	SEI	103	SEI	104	SEI	105	SEI	106	SEI	107	SEI	108	SEI	109	SEI	110	SEI	111	SEI	112	SEI	113	SEI	114	SEI	115	SEI	116	SEI	117	SEI	118	SEI	119	SEI	120	SEI	121	SEI	122	SEI	123	SEI	124	SEI	125	SEI	126	SEI	127	SEI	128	SEI	129	SEI	130	SEI	131	SEI	132	SEI	133	SEI	134	SEI	135	SEI	136	SEI	137	SEI	138	SEI	139	SEI	140	SEI	141	SEI	142	SEI	143	SEI	144	SEI	145	SEI	146	SEI	147	SEI	148	SEI	149	SEI	150	SEI	151	SEI	152	SEI	153	SEI	154	SEI	155	SEI	156	SEI	157	SEI	158	SEI	159	SEI	160	SEI	161	SEI	162	SEI	163	SEI	164	SEI	165	SEI	166	SEI	167	SEI	168	SEI	169	SEI	170	SEI	171	SEI	172	SEI	173	SEI	174	SEI	175	SEI	176	SEI	177	SEI	178	SEI	179	SEI	180	SEI	181	SEI	182	SEI	183	SEI	184	SEI	185	SEI	186	SEI	187	SEI	188	SEI	189	SEI	190	SEI	191	SEI	192	SEI	193	SEI	194	SEI	195	SEI	196	SEI	197	SEI	198	SEI	199	SEI	200	SEI	201	SEI	202	SEI	203	SEI	204	SEI	205	SEI	206	SEI	207	SEI	208	SEI	209	SEI	210	SEI	211	SEI	212	SEI	213	SEI	214	SEI	215	SEI	216	SEI	217	SEI	218	SEI	219	SEI	220	SEI	221	SEI	222	SEI	223	SEI	224	SEI	225	SEI	226	SEI	227	SEI	228	SEI	229	SEI	230	SEI	231	SEI	232	SEI	233	SEI	234	SEI	235	SEI	236	SEI	237	SEI	238	SEI	239	SEI	240	SEI	241	SEI	242	SEI	243	SEI	244	SEI	245	SEI	246	SEI	247	SEI	248	SEI	249	SEI	250	SEI	251	SEI	252	SEI	253	SEI	254	SEI	255	SEI	256	SEI	257	SEI	258	SEI	259	SEI	260	SEI	261	SEI	262	SEI	263	SEI	264	SEI	265	SEI	266	SEI	267	SEI	268	SEI	269	SEI	270	SEI	271	SEI	272	SEI	273	SEI	274	SEI	275	SEI	276	SEI	277	SEI	278	SEI	279	SEI	28
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01 The present sequence for Mycobacterium tuberculosis (H3N2) from
 02 AAS05241 is 1 of 24 rpoB gene fragments (AAS05241-AAS05242) from
 03 various Mycobacterium species. These rpoB gene fragments can be used
 04 for diagnosis and identification of Mycobacterium species using a
 05 PCR-restriction fragment length polymorphism analysis (RFLP)
 06 method. The method comprises obtaining a restriction fragment length
 07 polymorphism (RFLP) pattern of the 24 rpoB gene fragments; isolating,
 08 amplifying and digesting the DNA fragment from the microorganism to
 09 fragments with the unidentified fragment. The rpoB gene fragments
 10 are useful to identify a wide range of Mycobacterium species, e.g., for
 11 diagnosis or to obtain epidemiological and pathogenesis information for
 12 selection of appropriate therapies, including M. tuberculosis, M. leprei
 13 and non-tuberculous mycobacteria (NTM) encountered in subjects infected
 14 with human immunodeficiency virus (HIV). Analysis of the rpoB gene
 15 fragments is rapid, precise, simple and cost effective (only 1 PCR
 16 required), and can differentiate between many species in a single
 17 experiment, including those difficult to distinguish by usual biochemical
 18 tests. Also described are oligonucleotide probes (AAS0527-AAS0542) for
 19 detecting specific Mycobacterium species.

20 Sequence: 214 BP; 49 A; 65 C; 70 G; 27 T; 0 other;
 21 Query Match: 100.00; Score: 26; 146 247; Length: 214;
 22 Best Local Similarity: 100.00; Prod. No. 12;
 23 Matches: 20; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

24 1. AATCTTCTTTCGACGACATCA 26
 25 2. TTTTCTTCTTCTTCTTCTTCTT
 26 3. TTTTCTTCTTCTTCTTCTTCTT
 27 4. TTTTCTTCTTCTTCTTCTTCTT

28 1. AATCTTCTTTCGACGACATCA 26
 29 2. TTTTCTTCTTCTTCTTCTTCTT
 30 3. TTTTCTTCTTCTTCTTCTTCTT
 31 4. TTTTCTTCTTCTTCTTCTTCTT

32 1. AATCTTCTTTCGACGACATCA 26
 33 2. TTTTCTTCTTCTTCTTCTTCTT
 34 3. TTTTCTTCTTCTTCTTCTTCTT
 35 4. TTTTCTTCTTCTTCTTCTTCTT

36 1. AATCTTCTTTCGACGACATCA 26
 37 2. TTTTCTTCTTCTTCTTCTTCTT
 38 3. TTTTCTTCTTCTTCTTCTTCTT
 39 4. TTTTCTTCTTCTTCTTCTTCTT

40 1. AATCTTCTTTCGACGACATCA 26
 41 2. TTTTCTTCTTCTTCTTCTTCTT
 42 3. TTTTCTTCTTCTTCTTCTTCTT
 43 4. TTTTCTTCTTCTTCTTCTTCTT

44 1. AATCTTCTTTCGACGACATCA 26
 45 2. TTTTCTTCTTCTTCTTCTTCTT
 46 3. TTTTCTTCTTCTTCTTCTTCTT
 47 4. TTTTCTTCTTCTTCTTCTTCTT

48 1. AATCTTCTTTCGACGACATCA 26
 49 2. TTTTCTTCTTCTTCTTCTTCTT
 50 3. TTTTCTTCTTCTTCTTCTTCTT
 51 4. TTTTCTTCTTCTTCTTCTTCTT

52 1. AATCTTCTTTCGACGACATCA 26
 53 2. TTTTCTTCTTCTTCTTCTTCTT
 54 3. TTTTCTTCTTCTTCTTCTTCTT
 55 4. TTTTCTTCTTCTTCTTCTTCTT

56 1. AATCTTCTTTCGACGACATCA 26
 57 2. TTTTCTTCTTCTTCTTCTTCTT
 58 3. TTTTCTTCTTCTTCTTCTTCTT
 59 4. TTTTCTTCTTCTTCTTCTTCTT

60 1. AATCTTCTTTCGACGACATCA 26
 61 2. TTTTCTTCTTCTTCTTCTTCTT
 62 3. TTTTCTTCTTCTTCTTCTTCTT
 63 4. TTTTCTTCTTCTTCTTCTTCTT

64 polynorphism (RFLP) pattern of the 24 rpoB gene fragments; isolating,
 65 amplifying and digesting the DNA fragment from the microorganism to
 66 fragments with the unidentified fragment. The rpoB gene fragments
 67 are useful to identify a wide range of Mycobacterium species, e.g., for
 68 diagnosis or to obtain epidemiological and pathogenesis information for
 69 selection of appropriate therapies, including M. tuberculosis, M. leprei
 70 and non-tuberculous mycobacteria (NTM) encountered in subjects infected
 71 with human immunodeficiency virus (HIV). Analysis of the rpoB gene
 72 fragments is rapid, precise, simple and cost effective (only 1 PCR
 73 required), and can differentiate between many species in a single
 74 experiment, including those difficult to distinguish by usual biochemical
 75 tests. Also described are oligonucleotide probes (AAS0527-AAS0542) for
 76 detecting specific Mycobacterium species.

77 Sequence: 214 BP; 49 A; 65 C; 70 G; 27 T; 0 other;
 78 Query Match: 100.00; Score: 26; 146 247; Length: 214;
 79 Best Local Similarity: 100.00; Prod. No. 12;
 80 Matches: 20; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

81 1. AATCTTCTTTCGACGACATCA 26
 82 2. TTTTCTTCTTCTTCTTCTTCTT
 83 3. TTTTCTTCTTCTTCTTCTTCTT
 84 4. TTTTCTTCTTCTTCTTCTTCTT

85 1. AATCTTCTTTCGACGACATCA 26
 86 2. TTTTCTTCTTCTTCTTCTTCTT
 87 3. TTTTCTTCTTCTTCTTCTTCTT
 88 4. TTTTCTTCTTCTTCTTCTTCTT

89 1. AATCTTCTTTCGACGACATCA 26
 90 2. TTTTCTTCTTCTTCTTCTTCTT
 91 3. TTTTCTTCTTCTTCTTCTTCTT
 92 4. TTTTCTTCTTCTTCTTCTTCTT

93 1. AATCTTCTTTCGACGACATCA 26
 94 2. TTTTCTTCTTCTTCTTCTTCTT
 95 3. TTTTCTTCTTCTTCTTCTTCTT
 96 4. TTTTCTTCTTCTTCTTCTTCTT

97 1. AATCTTCTTTCGACGACATCA 26
 98 2. TTTTCTTCTTCTTCTTCTTCTT
 99 3. TTTTCTTCTTCTTCTTCTTCTT
 100 4. TTTTCTTCTTCTTCTTCTTCTT

101 1. AATCTTCTTTCGACGACATCA 26
 102 2. TTTTCTTCTTCTTCTTCTTCTT
 103 3. TTTTCTTCTTCTTCTTCTTCTT
 104 4. TTTTCTTCTTCTTCTTCTTCTT

105 1. AATCTTCTTTCGACGACATCA 26
 106 2. TTTTCTTCTTCTTCTTCTTCTT
 107 3. TTTTCTTCTTCTTCTTCTTCTT
 108 4. TTTTCTTCTTCTTCTTCTTCTT

109 1. AATCTTCTTTCGACGACATCA 26
 110 2. TTTTCTTCTTCTTCTTCTTCTT
 111 3. TTTTCTTCTTCTTCTTCTTCTT
 112 4. TTTTCTTCTTCTTCTTCTTCTT

113 1. AATCTTCTTTCGACGACATCA 26
 114 2. TTTTCTTCTTCTTCTTCTTCTT
 115 3. TTTTCTTCTTCTTCTTCTTCTT
 116 4. TTTTCTTCTTCTTCTTCTTCTT

117 1. AATCTTCTTTCGACGACATCA 26
 118 2. TTTTCTTCTTCTTCTTCTTCTT
 119 3. TTTTCTTCTTCTTCTTCTTCTT
 120 4. TTTTCTTCTTCTTCTTCTTCTT

121 1. AATCTTCTTTCGACGACATCA 26
 122 2. TTTTCTTCTTCTTCTTCTTCTT
 123 3. TTTTCTTCTTCTTCTTCTTCTT
 124 4. TTTTCTTCTTCTTCTTCTTCTT

[illegible][illegible][illegible]

[illegible]

XX New pair of polymerase chain reaction (PCR) primers for
 XX sequence specific amplification of the rpoB gene from mycobacterial
 XX species useful for detecting and identifying mycobacterial species
 XX (Page 7; Page 63-64; 94pp; English)
 XX This sequence represents a mycobacterial rpoB gene fragment that is
 XX amplified using the PCR primers of the invention. The primers form a
 XX sequence tree for identifying mycobacterial species by constructing
 XX a phylogenetic tree for the species. The use of the primers for
 XX sequence specific amplification of the rpoB gene (encoding the beta
 XX subunit of RNA polymerase) from mycobacterial species provides an
 XX efficient way of characterising these species. In addition, to
 XX phylogenetic analysis, the rpoB gene can be used as an alternative to
 XX the 16S rRNA gene because it has four subunits, which are highly
 XX conserved throughout prokaryotes. The method is particularly useful for
 XX species which lack regions of unambiguously identifiable mycobacterial DNA. Finally,
 XX susceptibility can be simultaneously determined in M. tuberculosis
 XX Sequence: 506 bp; 50 A; 109 G; 101 C; 46 T; 9 other;
 XX Query Match: 100.0%; Score 24; 100 bp; Length: 24
 XX Best Local Similarity: 100.0%; Pred. No. 0.27;
 XX Matches: 24; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0
 XX
 XX 1 AAGGATGACGCGGAGGAGGCA 24
 XX 1111111111111111111111
 XX 100 AAGGATGACGCGGAGGAGGCA 277
 XX
 XX RESULT 8
 XX AAX27100%
 XX 10 AAX27100 standard; (NA) 506 bp;
 XX AAX27100;
 XX 27 MAY 1999 (first entry)
 XX 27 MAY 1999 (first entry)
 XX RpoB gene fragment
 XX RpoB gene mycobacterial phylogenetic tree construction
 XX mycobacterial species identification; phylogenetic analysis; ss;
 XX Mycobacterial bevis;
 XX Woese et al. 1990;
 XX 04 FEB 1999;
 XX 28 JUL 1999; 98K; 0045501;
 XX 29 JUL 1999; 98K; 0045501;
 XX (KON) 10 NUBB 1999;
 XX Kim R. Kook Y;
 XX W. Lee 5/9/97/16;
 XX New pair of polymerase chain reaction (PCR) primers for
 XX sequence specific amplification of the rpoB gene from mycobacterial
 XX species useful for detecting and identifying mycobacterial species
 XX (Page 7; Page 63-64; 94pp; English)
 XX This sequence represents a mycobacterial rpoB gene fragment that is
 XX amplified using the PCR primers of the invention. The primers form a
 XX sequence tree for identifying mycobacterial species by constructing
 XX a phylogenetic tree for the species. The use of the primers for
 XX sequence specific amplification of the rpoB gene (encoding the beta
 XX subunit of RNA polymerase) from mycobacterial species provides an
 XX efficient way of characterising these species. In addition, to
 XX phylogenetic analysis, the rpoB gene can be used as an alternative to
 XX the 16S rRNA gene because it has four subunits, which are highly
 XX conserved throughout prokaryotes. The method is particularly useful for
 XX species which lack regions of unambiguously identifiable mycobacterial
 XX DNA. Finally, susceptibility can be simultaneously determined in M.
 XX tuberculosis
 XX Sequence: 506 bp; 50 A; 109 G; 101 C; 46 T; 9 other;
 XX Query Match: 100.0%; Score 24; 100 bp; Length: 24
 XX Best Local Similarity: 100.0%; Pred. No. 0.27;
 XX Matches: 24; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0
 XX
 XX 1 AAGGATGACGCGGAGGAGGCA 24
 XX 1111111111111111111111
 XX 100 AAGGATGACGCGGAGGAGGCA 277
 XX

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 XX 1111111111111111111111
 XX 100 AAGGATGACGCGGAGGAGGCA 277
 XX
 XX RESULT 8
 XX AAX27100%
 XX 10 AAX27100 standard; (NA) 506 bp;
 XX AAX27100;
 XX 27 MAY 1999 (first entry)
 XX 27 MAY 1999 (first entry)
 XX RpoB gene fragment
 XX RpoB gene mycobacterial phylogenetic tree construction
 XX mycobacterial species identification; phylogenetic analysis; ss;
 XX Mycobacterial bevis;
 XX Woese et al. 1990;
 XX 04 FEB 1999;
 XX 28 JUL 1999; 98K; 0045501;
 XX 29 JUL 1999; 98K; 0045501;
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[illegible][illegible]

